STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

Pre-Grant Pub. only

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/779,418PA
Source: IFW16
Date Processed by STIC: 4/19/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 10/779,418PA

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ✓ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFW16

RAW SEQUENCE LISTING DATE: 04/19/2005
PATENT APPLICATION: **US/10/779,418PA** TIME: 10:40:27

Input Set : **N:\efs\10779418_efs_pgpub\pto.amc.txt**
Output Set: **N:\CRF4\04192005\J779418PA.raw**

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      4 <110> APPLICANT: Bisgard Frantzen, Henrik
      5       Svendsen, Allan
      6       Borchert, Torben Vedel
      8 <120> TITLE OF INVENTION: Amylase Variants
     11 <130> FILE REFERENCE: 4318.224 US
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/779,418PA
C--> 13 <141> CURRENT FILING DATE: 2004-02-12
     13 <150> PRIOR APPLICATION NUMBER: 09/902,188
     14 <151> PRIOR FILING DATE: 2001-07-10
     16 <150> PRIOR APPLICATION NUMBER: 08/600,656
     17 <151> PRIOR FILING DATE: 1996-02-13
     19 <150> PRIOR APPLICATION NUMBER: PCT/DK96/00056
     20 <151> PRIOR FILING DATE: 1996-02-05
     22 <150> PRIOR APPLICATION NUMBER: Denmark
     23 <151> PRIOR FILING DATE: 1995-02-03
W--> 25 <150> PRIOR APPLICATION NO: Denmark
     26 <151> PRIOR FILING DATE: 1995-03-29
W--> 28 <150> PRIOR APPLICATION NO: Denmark
     29 <151> PRIOR FILING DATE: 1995-09-29
W--> 31 <150> PRIOR APPLICATION NO: Denmark
     32 <151> PRIOR FILING DATE: 1995-10-06
E--> 34 <160> NUMBER OF SEQ ID NOS: 32
     36 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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insufficient - give serial numbers (application nos.)

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

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     38 <210> SEQ ID NO: 1
E--> 40 <211> LENGTH:
E--> 40 <212> TYPE:
E--> 40 <213> ORGANISM:
     40 <400> SEQUENCE: 1
     43 (2) INFORMATION FOR SEQ ID NO: 1:
     45      (i) SEQUENCE CHARACTERISTICS:
     46           (A) LENGTH: 485 amino acids
     47           (B) TYPE: amino acid
     48           (C) STRANDEDNESS: single
     49           (D) TOPOLOGY: linear
     51     (ii) MOLECULE TYPE: peptide
     53     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     55      His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
     56      1               5                  10                  15
     58      Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
```

(see p2)

10/779,418 PA

SEQUENCE LISTING

see items 1 and 4 on Error Summary Sheet

<110> Bisgard Frantzen, Henrik
Svendsen, Allan
Borchert, Torben Vedel

<120> Amylase Variants

<130> 4318.224 US

<140> 09/902,188
<141> 2001-07-10

<150> 08/600,656
<151> 1996-02-13

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<151> 1996-02-05

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<151> 1995-02-03

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<150> Denmark
<151> 1995-09-29

<150> Denmark
<151> 1995-10-06

<160> 32

<170> FastSEQ for Windows Version 3.0

<210> 1

<400> 1

← This is "new" Sequence Rules format.

DO not combine "new" and "old" formats. Use entirely "old" or entirely "new"

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

← This is "old" Sequence Rules format

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr

(The above is a sample of global errors